Claims

Amendments to the Claims

1. – 29. (Canceled)

30. (Currently Amended) A method of determining the quinolone resistance of an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli, Citrobacter freundii, Enterobacter aerogenes, Enterobacter cloacae, Klebsiella oxytoca, Klebsiella Pneumoniae, Providencia stuartii* and *Serratia marcescens* in a sample, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid [[of]] sequence set forth as one of SEQ ID NOS:9-16, or a complementary sequence thereof, respectively, the presence of hybridization with a nucleic acid indicating the quinolone susceptibility of the respective species.

31. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:9, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Escherichia coli* in the sample.

32. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:10, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Citrobacter freundii* in the sample.

33. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:11, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Enterobacter aerogenes* in the sample.

34. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:12, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Enterobacter cloacae* in the sample.

35. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:13, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Klebsiella oxytoca* in the sample.

36. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:14, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Klebsiella pneumoniae* in the sample.

37. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:15, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Providencia stuartii* in the sample.

38. (Withdrawn) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:16, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Serratia marcescens* in the sample.

39. (Currently Amended) The method of claim 30, wherein ~~hybridation~~hybridization of the probe to the nucleic acid sequence of SEQ ID NOs: 1-9 indicates that the Enterobacteriaceae species is susceptible to quinolone and a one or more base pair mismatch of the probe to the nucleic acid sequence of one or more of SEQ ID NOs: 1-9 indicates that Enterobacteriaceae species is resistant to quinolone.

40. (Previously Presented) The method of claim 30, wherein the probe is from about 10 to 50 nucleotides in length.

41. (Previously Presented) The method of claim 30, wherein the probe consists of the nucleic acid sequence set forth as one of SEQ ID NOs: 25-33.

42. (New) The method of claim 30, wherein the probe selectively hybridizes to nucleotides 25 to 613 of SEQ ID NO: 9.

43. (New) The method of claim 42, wherein the probe selectively hybridizes to nucleotides 199 to 318 of SEQ ID NO:9, or a complementary sequence thereof.

44. (New) The method of claim 42, wherein the probe selectively hybridizes to nucleotides 239 to 663 of SEQ ID NO: 9, or a complementary sequence thereof.

44. (New) The method of claim 30, wherein the probe is about 25 nucleotides in length.

45. (New) The method of claim 44, wherein the probe is from about 10 to 50 nucleotides in length.

45. (New) The method of claim 44, wherein the probe is about 25 nucleotides in length.

46. (New) The method of claim 30, wherein the method comprises the use of a polymerase chain reaction (PCR), ligase chain reaction, or a nucleotide array.

47. (New) The method of claim 30, wherein the probe is labeled.

48. (New) The method of claim 30, wherein the nucleic acid sequence set forth as SEQ ID NO: 9 is amplified prior to combining the sample with the nucleic acid probe.